

The erythromycin PKS

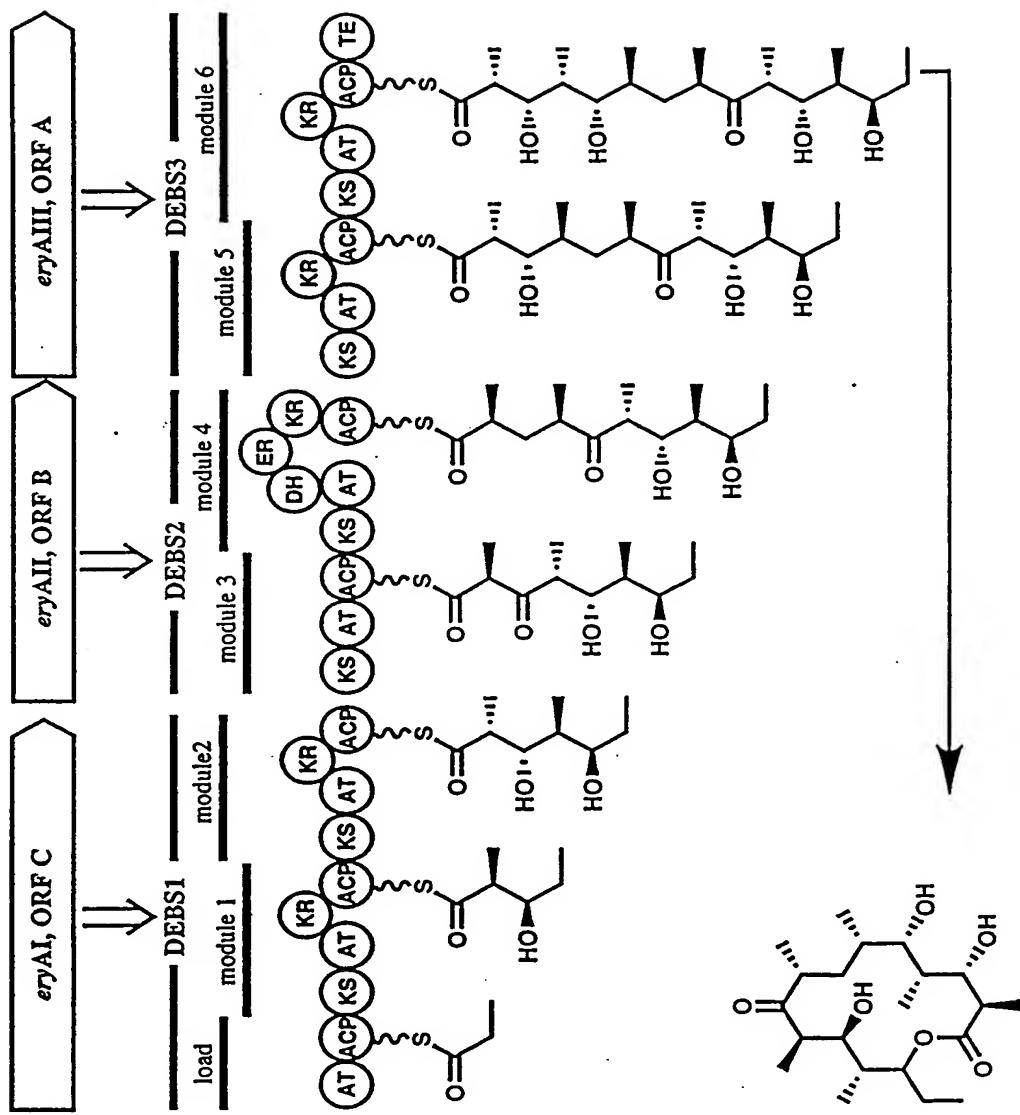


Fig. 1

2/12

KCLFDAU
KCLFPEU
KCLFACT
KCLFHIR
KCLFGRA
KCLFMNOG
KCLFTCM
KCLFCIN
KCLFVNZ
KCLFWHIE
KSGRA
KSHIR
KSACT
KSCIN
KSVNZ
KSNOG
KSTCM
KSDAU
KSPEU
KSWHI

MVITGLGIVAPNGLVGAIWDAVLNGRNGIGPLR
MTGTAARTASSQLHASPAGRGLRGRAVVTGLGIVAPNGLVGAYWDAVLNGRNGIGPLR
MSVLITGVGVVAPNGLGLAPYWSAVLDGRHGLGPVTT
MSTWVTGMGVVAPNGLGADDHWAATLKGHRGISRLS
MSTPDRRAVVTGLSVAAPGGLGTERYWKSLLTGENGIAELS
MTAAVVTGLGVVAPTGLGVREHWSSTVRGASAIGPVT
MSAPAPVVTGLGIVAPNGTGTTEEYWAATLAGKSGIDVIQ
MTP-VAVITGMGIAAPNGLGRPTTGRPPWAPRAASAAST
MSA5VVTGLGVAAPNGLGREDFWASTLGGKSGIGPLT
MSGPQRTGTGGGSRAAVTGLGVLSPHGTGVEAHWKAADGTSSLGPVTT
MTRRVVITGVGVRAVPGGSGTKEFWDLTTAGRTATRPI
MTRRVVITGVGVRAVPGGLGAKNFWELLTSGRTAATTRIS
MKRRVVITGVGVRAVPGGNGTRQFWELLTSGRTAATTRIS
MTQRRAVTAITGIEVLAPOGLGRKEFWQLLSEGRTATRGIT
MTARRVVITGIEVLAPOGGTSKAFWNLSEGRTATRGIT
MKESINRRVVITGIGIVAPDATGVKPFWDLLTAGRTATRTIT
MTRHAERKVITGIGVRAVPGGAGTAAFWDLTTAGRTATRTIS
MNRRVVITGMGVVAPGAIGIKSFWELLSEGTTATRAIT
MNRRIVITGIGVVAAPGAVGTKPFWDLLSEGTTATRAIS
MTRRRVAVITGIGVVAAPGGIGTPOFWRLSEGRTATRIS

KCLFDAU
KCLFPEU
KCLFACT
KCLFHIR
KCLFGRA
KCLFNOG
KCLFTCM
KCLFCIN
KCLFVNZ
KCLFWHIE
KSGRA
KSHIR
KSACT
KSCIN
KSVNZ
KSNOG
KSTCM
KSDAU
KSPEU
KSWHI

RFDADDGRLGRLAGEVSDFVP-EDHLPKRLLVQTDPMQTALAAAEEWALREAGCAPSS--
RFTGDGRLGRLAGEVSDFVP-EDHLPKRLLAQTDPMTQY-ALAAAEEWALRESQCPSS--
RFDVSRYPATLAGQIDDFHA-PDHI PGRLLPQTDPMSTR-ALTAADWALQDAKADPES-L
RFDPTGYPAELAGQVLDFDA-TEHLPKRLLPQTDVSTRF-ALAAAAWALADAEVDPAE-L
RFDASRYPSRLAGQIDDFEA-SEHLP SRLLPQTDVSTRY-ALAAADWALADAGVGPGESGL
RFDAGRYP SKLAGEVPGFVP-EDHLP SRLMPQTDHMTRL-ALVAADWAFQDAAVDPSK-L
RFDPHGYPVRVGGEVLAFDA-AAHLPGRLLPQTDRMTOH-ALVAEEWALADAGLEPEK-Q
RFDPSGYPAQLAGEIPGFRA-AEHLPGRLVPQTDRTVTRL-SLAAADWALADAGVEVAA-F
RFDPTGYPARLAGEVPGFAA-EEHLP SRLLPQTDRMTRL-ALVAADWALADAGVRPEE-Q
REGCAHILPLRVAGEVHGFDAA-ETVEDRFLVQTDRTFH-ALSATQHALADARFGRADWD
FFDASPFRSRIAGEI-DFDAVAEGFSPREVRRMDRATQF-AVACTRDALADSGLDTGA-L
FFDPTPNRSQIAAEC-DFDPEHEGLSPREIRRMDRAAQF-AVVCTRDAVADSGLEFEQ-V
FFDPSPYRSQVAAEA-DFDPVAEGFGPRELDRMDRASQF-AVACAREFAASGLDPDT-L
FFDPAPFRSKVAAEA-DFCGLENGLSPQEVRMDRAAQF-AVVTAR-AVEDSGAELAA-H
FFDPTPFRSRVAAEI-DFDPEAHGLSPQEIRRMDRAAQF-AVVAAR-AVADSGIDLAA-H
AFDPSPFRSRIAAEC-DFDPLAEGLTPQQIRRMDRATQF-AVVSARESLEDSGLDLGA-L
LFDAAPYRSRIAGEI-DFDPIGEGLSPRQASTYDRATQL-AVV CAREALKDSGLDPAA-V
TFDATPFRSRVAAEC-DFDPVAAGLSAEQARRLDRAGQF-ALVAGQEALTDSGLRIGE-D
TFDATPFRSRVAAEC-DFDPVAAGLSAEQARRLDRAGQF-ALVAGQEALADSGLRIDE-D
LFDPGSLRSQIAAEC-DFEPSPDHGLGLATAORCDRYVOE-ALVAASEAVRDANI DMNR-E

Fig 2A

KCLFDAU	-PLEAGVITASASGGFASQRELQNLWSKG-----PAHVSAYMSFAWFY-AVNIGQIAIR
KCLFPEU	-PLEAGVITASASGGFAFGQRELQNLWSKG-----PAHVSAYMSFAWFY-AVNIGQIAIR
KCLFACT	TDYDMGVVTANACGGFDFTREFRKLWSEG-----PKSVSVYESFAWFY-AVNIGQISIR
KCLFHIR	PEYGTGVTITSNATGGFEFTIREFRKLWQAQG-----PEFVSVYESFAWFY-AVNIGQISIR
KCLFGRA	DDYDLGVVTSTAQGGFDFTIREFHKLWLSQG-----PAYVSVYESFAWFY-AVNIGQISIR
KCLFN0G	PEYGVGVVTASSAGGFEGFIRELQNLWLSG-----PQVVSAYQSFAWFY-AVNIGQVSIR
KCLFTCM	DEYGLGVLTAAAGAGGFEGFQREMOKLWGTG-----PERVSAYQSFAWFY-AVNIGQISIR
KCLFCIN	DPLDMGVVTASHAGGFEGFQDELOKLLGQG-----QPVL SAYQSFAWFY-AVNSGQISIR
KCLFVNZ	DDFDMDGVVTASASGGFEGFQGELOKLLWLSQG-----SQVVSAYQSFAWFY-AVNSGQISIR
KCLFWHIE	SPYSGVVTAAAGCGGGEGFQRELQNLWGHG-----SRHVGPYQSIAWFY-AASTGQVSIR
KSGRA	DPSRIGVALGSAVASATSLENEYLVMSDSGREWLVDPAHLSPMMDYLSPGVMPAEVAWA
KSHIR	PPERIGVSLGSAVAATSLLEQEYLVLSDGGREWQVDPAYLSAHMFMDYLSPGVMPAEVAWT
KSACT	DPARVGVSLSGSAVAATSLEREYLLLSDSGRDWEVDAWLRSRHMFDYLVPSVMPAEVAWA
KSCIN	PPHRIGVVGSAGVATMGLDNEYRVSVDGGRLLDVLVDHRYAVPHLYNVLVPPSSFAAEVAWA
KSVNZ	DPYRVGVTVGSAVGATMGLDEEYRVSVDGGRLLDVLVDHAYAVPHLYDYMVPSSFAAEVAWA
KSN0G	DASRTGVVVGSAVGCTTSLEEEYAVVSDGRNWLVDDGYAVPHLFDYFVPPSSIAAEVAHD
KSTCM	NPERIGVSI GTAVGCTTGLDREYARVSEGGSRWLVDHTLAVEQLFDYFVPTSI CREV AWE
KSDAU	SAHRVGVCVGTAVGCTQKLESEYVALSAGGANVVDPHRGAPELYDYFVPPSSLAAEVAWL
KSPEU	SAHRVGVCVGTAVGCTQKLESEYVALSAGGAHVVDPGRGSPELYDYFVPPSSLAAEVAWL
KSWHI	DPWRAGATLGTAVGGTRLEHDYVLVSEGRSRWDVDRRSEPHERAFTPATLSSAVAEE

KCLFDAU	-HDLRGPVGVVVAEQAGGLDALAHAR-RKVRGGAE-LIVSGAMDSSLCP-YGMAAQVRSG
KCLFPEU	-HDLRGPVGVVVAEQAGGLDALAHAR-RKVRGGAE-LIVSGAVDSSLCP-YGMAAQVKSG
KCLFACT	-HGMRGPSALVAEQAGGLDALGHAR-RTIRRGTP-LVSGGVDALDP-WGVVSQIASG
KCLFHIR	-HGLRGPGSVLVAEQAGGLDAIGHAR-RTVRRGPG-WCSAVASTRSTR-GASSSQLSGG
KCLFGRA	-NTMRGPAALVGEQAGGLDAIGHAR-RQLRRGLP-MVVAVGAVDGSPCP-WGVVAQLSSG
KCLFN0G	-HGLRGPGGVLVTEQAGGLDALQAR-RQLRRGLP-MVVAVGAVDGSPCP-WGVVAQLSSG
KCLFTCM	-HGMRGHSSVFVTEQAGGLDAAAHAAR-RLLRKGTLNTALTGGCEASLCP-WGLVAQIPSG
KCLFCIN	-HGMKGPSGVVSDQAGGLDALAQAR-RLVRKGTP-LIVCGAVEPRSAPGAGSPSSPAGG
KCLFVNZ	-NGMKGPSGVVSDQAGGLDAVAQAR-RQIRKGTR-LIVSGGVDASLCP-WGVVAHVASD
KCLFWHIE	-NDFKPGCVAADEAGGLDALAHAA-LAVRNGTD-TVVGATEAPLAP-YSIVCQLGYP
KSGRA	-AGAECPVIMVSDGCTSGLDVGYAV-QGTREGSADVVVAGAADTPVSPIVVACFDAIKA
KSHIR	-VGAEGPVAMVSDGCTSGLDLSHAC-SLIAEGTIDVMVAGAADTPITPIVSCFDAIKA
KSACT	-VGAEGPVIMVSTGCTSGLDVGNAV-RAIEEGSADVMFAGAADTPITPIVACFDAIKA
KSCIN	-VGAEGPSTVSTGCTSGIDAVGIAV-ELVREGSDVDMVAGADVAPISPIP-CVLFDAIKA
KSVNZ	-VGAEGPNTVSTGCTSGLDVGYARGLREGSADVMIAGSSDAPISIPITMACFDAIKA
KSN0G	RIGAEGPVLVSTGCTSGLDAVGRAA-DLIAEGAADMLAGATEAPISIPITVACFDAIKA
KSTCM	-AGAEGPVTVSTGCTSGLDAVGYGT-ELIRDGRADVVVCGATDAPISIPITVACFDAIKA
KSDAU	-AGAEGPVNIVSAGCTSGIDSIGYAC-ELIREGTVDVMLAGGVDAPIAPITVACFDAIRV
KSPEU	-AGAEGPVNIVSAGCTSGIDSIGYAC-ELIREGTVDAMVAGGVDAPIAPITVACFDAIRV
KSWHI	-FGVRGPVQTVSTGCTSGLDAVGYAY-HAVAEGRVDVCLAGAADSPISIPITMACFDAIKA

KCLFDAU	RLSGSDDPTAGYLPFDRAAGHVPGEGL-GAILAVEDAERVAERG-GKVYGSIAGT-ASFD
KCLFPEU	RLSGSDNPTAGYLPFDRAAGHVPGEGL-GAILTVEDAERAERG-AKVYGSIAGYGASFD
KCLFACT	RISTATDPDRAYLPFDERAAGYVPGEGL-GAILVLEDAAAERGRHDAYGELACCASTFD
KCLFHIR	RVSRAZDPGRAYLPFDVAANGYVPGEGL-GAILLLEDAESAKARG-ATGYGEIAGYAATFD
KCLFGRA	LVSTVADPERAYLPFDVADASGYVPGEGL-GAVLIVEDADSARARG---AERIYVRSPLRRD
KCLFN0G	GLSTSDPRRAYLPFDAAAGGHPGEGL-GALLVLESDESARARGVTRWYGRIDGYAATFD
KCLFTCM	FLSEATDPHDAYLPFDARAAGYVPGEGL-GAMLVAERADSARERDAATVYGRIGHASTFD
KCLFCIN	-MSDSDEPNRAYLPFDRDGRGYVPGGGRGVVPLERAEAAPARG-AEVYGE-AGPLARL-
KCLFVNZ	RLSTSEEPARGYLPFDREAQGHVPGEGL-GAILVMEAAAERERG-ARIYGEIAGYGSTFD
KCLFWHIE	ELSRATEPDRAYRPFTEAACGFAPAEG-GAVLVVEEEAAERERG-ADVRATVAGHAATFT

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KSGRA	TTPRNDDPAHASRPFDGTRNGFVLAEG-AAMFVLEEYEAQRRG-AHIYAEVGGYATRSQ
KSHIR	TTPRNDDPEHASRPFDNSRNGFVLAEG-AALFVLEELEHARARG-AHVYAEISGCATRLN
KSACT	TTARNDDPEHASRPFDGTRDFVLAEG-AAMFVLEDYDSALARG-ARIHAEISGYATRCN
KSCIN	TPPRHDAPATASRPFDSTRNGFVLGEG-AAVFVLEELHSARRRG-AHIYAEIAGYATRSN
KSVNZ	TTNRYDDPAHASRPFDGTRNGFVLGEG-AAVFVLEELESARARG-AHIYAEIAGYATRSN
KSONG	TPPRNDTPAEASRPFDRTRNGFVLGEG-AAVFVLEEFEHARRRG-ALVYAEILAGFATRSN
KSTCM	TSANNDPAHASRPFDRNRDGFVLGEG-SAVFVLEELSAARRRG-AHAYAEVRGFATRSN
KSDAU	TSDHNDTPETLA-PFSRSRNGFVLGEG-GAIVVLEEAAVRRG-ARIYAEIGGYASRGN
KSPEU	TSDHNDTPETASRPFSSRSRNGFVLGEG-GAIVVLEEAAVRRG-ARIYAEIGGYASRGN
KSWHI	TSPNNDDPAHASRPFADRNFGVMGEG-AAVLVLEDLEHARARG-ADVYCEVSGYATFGN

* * *

KCLFDAU	-PPPGSGRP---SALARAVETALADAGLDRSDIAVVFADGAA-VGELDVAEAEALASVFG
KCLFPEU	-PPPGSGRP---SALARAVETALADAGLDGSIDIAVVFADGAA-VPELDAAEAEALASVFG
KCLFACT	-PAPGSGRP---AGLERAIRLALNDAGTGPEDVVFADGAG-VPELDAAEARAIGRVFG
KCLFHIR	-PAPGSRP---PALRRAIELALADELRPEQDVVFADGAG-VAELDAIEAAAIRELFG
KCLFGRA	-PAPGSGRP---PALGRAAEELALAEAGLTPADISVVFADGAG-VPELDRAEADTLARLFG
KCLFNOG	-PPPGSGRP---PNLLRAAQAAQALDDAEVGPEAVDVVFADASG-TPDEDAAEADAVRRLFG
KCLFTCM	-ARPGTGRP---TGPARAIRLAEEARVAPEDDVVFADASG-VPALDRAEAEALAEVFG
KCLFCIN	-PAPHSGRG---STRAHAIRTLADDAGTAPGDIRRVFADGGGRYPN-DRAEAEAISEVFG
KCLFVNZ	-PRPGSGRE---PGLRKAIELALADAGAAPGDDIDVVVFADASG-VPELDRVEAEALNAVFG
KCLFWHIE	GAGRWAESR---EGLARAIQGALAEAGCRPEEVDVVFADALG-VPEADRAEALALADALG
KSGRA	-AYHMTGLKKDGREMAESIRALDEARLDRTAVDVNAHGSG-TKQNDRHETAAFKRSLG
KSHIR	-AYHMTGLKTDGREMAEIRVALDLARIDPTIDYINAHGSG-TKQNDRHETAAFKRSLG
KSACT	-AYHMTGLKADGREMAETIRVALDESRTDATDIDYINAHGSG-TRQNDRHETAAFKRALG
KSCIN	-AYHMTGLR-DGAEMAEAIRLALDEARLNPEQDVYINAHGSG-TKQNDRHETAAFKKALG
KSVNZ	-AYHMTGLRPDGAEAEAIRVALDEARMNPTIEDYINAHGSG-TKQNDRHETAAFKKSLG
KSONG	-AYHMTGLRPDGAEAEAIRVALDEARMNPTIEDYINAHGSG-TKQNDRHETAAFKRSLG
KSTCM	-AYHMTGLRPDGAEAEAIRVALDEARMNPTIEDYINAHGSG-TKQNDRHETAAFKRSLG
KSDAU	-AYHMTGLRADGAEMAAIAITAAALDEARRDPSDVYINAHGTA-TRQNDRHETSAFKRSLG
KSPEU	-AYHMTGLRADGAEMAAIAITAAALDEARRDPSDVYINAHGTA-TKQNDRHETSAFKRSLG
KSWHI	-AYHMTGLTKEGLEMARAIIDLMAELDGSIAIDYINAHGSG-TQQNDRHETAAVKRSLG

. : : * * : : : * * * : : : * * : : : * *

Fig 2C

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KCLFDAU	P--HRVPVTVPKTLTGRLYSGAGPLDVTGLLALRDEVVPATGHVH-PDPDPLPLDVVTGCR
KCLFPEU	P--RRVPVTVPKTLTGRLYSGAGPLDVTALLALRDEVVPATAHVD-PDPDPLPLDVVTGCR
KCLFACT	R--EGVPVTVPKTTTGRLYSGGGPLDVTALMSLREGVIAPTAGVTSVPREYGIDLVLGCR
KCLFHIR	P--SGVPVTAPKTMGRLYSGGGPLDVLVAALLAIRDGVIPTVHTAEPVPEHQLDLVTGCR
KCLFGRA	P--RGVPVTAPKALTGRLCAGGGPADLAAALLALRDQVIPATGRHRAVPDAYALDLVTGCR
KCLFNOG	P--YGVPVTAPKTMGRLSAGGAALDVATALLALREGVVPPTVNVSRPRPEYELDLVLGCR
KCLFTCM	P--GAVPVTAPKTMGRLYAGGAALDVATALLSIRDCVVPPTVGTGAPAPGLGIDLVLHQ
KCLFCIN	P--GRVPVICPRTMTGRLHSGAPLDVACALLAMRAGVIPTVHID-PCPEYDLDLVLYQ
KCLFVNZ	T--GAVPVTAPKTMGRLYSGAPLDAAFLAMDEGVIPPTVNE-PDAAYGLDLVVGG
KCLFWHIE	PHAARVPVTAPKGTGRAYCAAVLDVTAVLAMEHGLIPPTPHVL--DVCHDLDLVTGCR
KSGRA	EHAYRVPVSSIKSMGGHSLGAIGSIEIAASVLAIEHNVPPTANLHTPDPECDDYVPLT
KSHIR	EHAYRTPVSSIKSMVGHSLGAIGSIEVAACALAEHGVPPTANLHEPDPECDDYVPLT
KSACT	EHARRTPVSSIKSMVGHSLGAIGSIEIAACVLALEHGVPPTANLRTSDPECDDYVPLT
KSCIN	EHAYRTPVSSIKSMVGHSLGAIGSIEIAASALAMEYDVVPPTANLHTPDPECDDYVPLT
KSVNZ	DHAYRTPVSSIKSMVGHSLGAIGSIEIAASALAMEHNVPPTGNLHTPDPECDDYVR-S
KSONG	DHAYRVPVSSIKSMIGHSLGAIGSIEIAASVLAITHDVVPPTANLHEPDPECDDYVPLR
KSTCM	QRAYDVPVSSIKSMIGHSLGAIGSIEIAACALAEHGVIPTANYEEDPPECDDYVPNV
KSDAU	DHAYRVPVSSIKSMIGHSLGAAGSLEVAATALAVEYGAIPPTANLHDPDPELDLDYVPLT
KSPEU	EHAYRVPVSSIKSMIGHSLGAVGSLEVAATALAVEYGVIPPTANLHDPDPELDLDYVPLT
KSWHI	EHAYATPMSSIKSMVGHSLGAIGSIEIAACVLAHAMHQVVPPTANYTTPDPECDDYVPRE

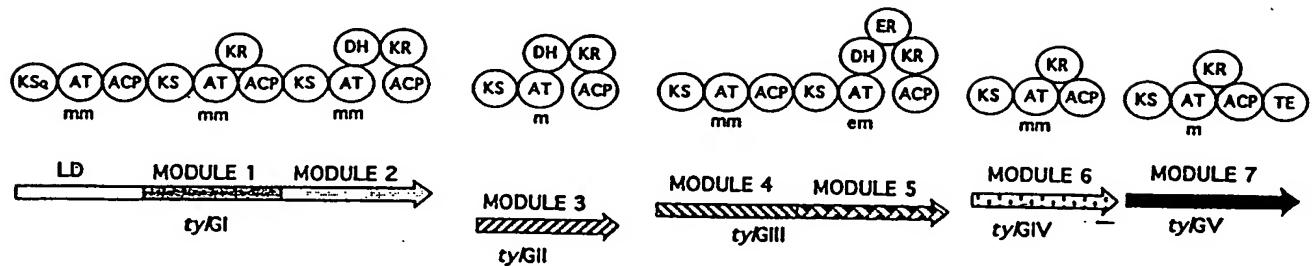
KCLFDAU	PRAMADARAALVVARGHGGFNSALVVRGAA-----
KCLFPEU	PRSLADARAALLVARGYGGFNSALVVRGAA-----
KCLFACT	PRSTAPRTA-LVLARGRWGFNSAABLRRFAPTP-----
KCLFHIR	PRHQQLGTA-LVLARGKWFNSAVVVRGVFIG-----
KCLFGRA	PREAALSAA-LVLARGRGFNSAVVTLRGSDHRRPT-----
KCLFNOG	PRRTPLARA-LVLARGRGFNAAMVVAGPRAETR-----
KCLFTCM	PRELRVDTA-LVVARQMGGFNSALVVRHG-----
KCLFCIN	VRPAALRTA-LGGARGHGGFNSALVVRAGQ-----
KCLFVNZ	PRTAEVNTA-LVIARGHGGFNSAMVVRSAN-----
KCLFWHIE	ARPAEPRTA-LVLARGLMGNSNSALVLRRGAVPPEGR-----
KSGRA	AREQRVDTV-LTVGSGFGGFQSAMVLHRPEAAA-----
KSHIR	AREQRVDTV-LSVGSFGGFQSAMVLRLGGANS-----
KSACT	ARERKLRSV-LTVGSGFGGFQSAMVLRDAETAGAAA-----
KSCIN	ARDQRVDSV-LTVGSGFGGFQSAMVLTSQ-----RSTV
KSVNZ	CREQLTDSV-LTVGSGFGGFQSAMVLARPE---RKIA
KSNOG	ARACPVDIV-LTVGSGFGGFQSAMVLCPGSRGRSAA
KSTCM	AREQRVDTV-LSVGSFGGFQSAAVLARPETRS-----
KSDAU	AREKVRHA-LTVGSGFGGFQSAMLLSRPER-----
KSPEU	AREKVRHA-LTVGSGFGGFQSAMLLSRLER-----
KSWHI	ARERTLHRV-LSVGSFGGFQSAVVLSGSEGGLR-----

mole: ~/ks2%

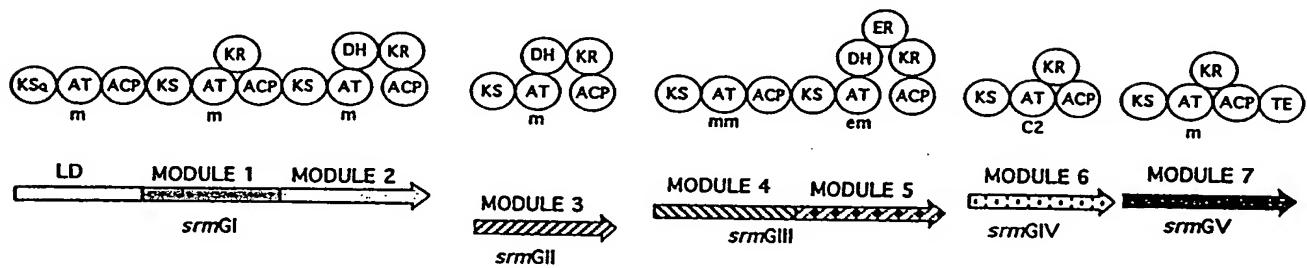
Fig 2D

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ORGANISATION OF THE TYLOSIN-PRODUCING POLYKETIDE SYNTHASE



ORGANISATION OF THE SPIRAMYCIN-PRODUCING POLYKETIDE SYNTHASE



ORGANISATION OF THE NIDAMYCIN-PRODUCING POLYKETIDE SYNTHASE

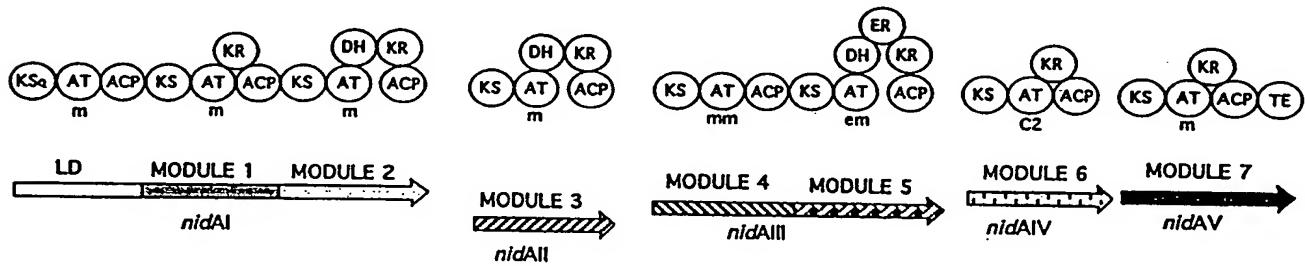


Fig 3

m: malonyl transferase
 mm: methylmalonyl transferase
 em: ethylmalonyl transferase
 C2: unknown C2 unit transferase

1	50	
niddamycin	-----	MAGHGDATAQ KAQDAEKSED GS DAI AVIGM
platenolide	-----	----- MS GELAISRSDD RSDAVAVVGM
monensin	-----	----- MAAS ASASPSGPSA GPDPIAVVGM
oleandomycin	-----	----- MHVPGEE NGHSIAIVGI
tylosin	MSSALRRAVQ	SNCGYGDLMT SNTAAQNTGD QEDVDGPDST HGGEIAVVGM
51		100
niddam...	SCRFPGAPGT AEFWQLLSSG	ADAVVTAADG RRR..... GTIDA
platenol.	ACRFPGAPGI AEFWKLTDG	RDAIGRDA DG RRR..... GMIEA
monensin	ACRLPGAPDP DAFWRLLSEG	RSAVSTAPPE RRRADSGLHG P...GGYLD R
oleandom	ACRLPGSATP QEFWRLLADS	ADALDEPPAG RFPTGSLSSP PAPRGGF LDS
tylosin	SCRLPGAAGV EEFWELLRSG	RGMPTRQDDG TWRAA..... LED
101		150
niddam...	PADFDAAFFG MSPREAAATD	PQQRLVLELG WEALEDAGIV PESLRGEAAS
platenol.	PGDFDAAFFG MSPREAAETD	PQQRLMLELG WEALEDAGIV PGSLRGEAVG
monensin	IDGFDADFFH ISPREAVAMD	PQQRLLELS WEALEDAGIR PPTLARSRTG
oleandom	IDTFDADFFN ISPREAGVLD	PQQRLALELG WEALEDAGIV PRHLRGTRTS
tylosin	HAGFDAGFFG MNARQAAATD	PQHRLMLELG WEALEDAGIV PGDLTGTDG
151		200
niddam...	VFVGAMNDDY ATLLH.RAGA	PTDTYTATGL QHSMIANRLS YFLGLRGPSL
platenol.	VFVGAMHDDY ATLLH.RAGA	PVGPHATGL QRMLANRLS YVLGTRGPSL
monensin	VFVGAFWDDY TDVNLNRAPG	AVTRHTMTGV HRSILANRIS YAYHLAGPSL
oleandom	VFMGAMWDDY AHLAHARGEA	ALTRHSLTGT HRGMIANRLS YALGLQGPSL
tylosin	VFAGVASDDY A.VLTRRS AV	SAGGYTATGL HRALAANRLS HFLGLRGPSL
201		250
niddam...	VVDTGQSSSL VAVALAVESL	RGGTSGIALA GGVNLVLAEE GS.AAMERVG
platenol.	AVDTAQSSSL VAVALAVESL	RAGTSRVAVA GGVNLVLADE GT.AAMERLG
monensin	TVDTAQSSSL VAVHLACESI	RSGDSDIAFA GGVNLICSPR TTELAAARFG
oleandom	TVDTGQSSSL AAVHMACESL	ARGESDLALV GGVNLVLDPA GT.TGVERFG
tylosin	VVDSAQSASL VAVQLACESL	RRGETSLAVA GGVNLILTEE ST.TVMERMG
251		300
niddam...	ALSPDGRCHT FDARANGYVR	GE GGAI VV LK PLADALADGD RVYCVVRGVA
platenol.	ALSPDGRCHT FDARANGYVR	GE GGAA VV LK PLADALADGD PVYCVVRGVA
monensin	GLSAAGRCHT FDARADGFVR	GE GGLV V LK PLAAARRDGD TVYCVIRGSA
oleandom	ALSPDGRCYT FDSRANGYAR	GE GGVV VV LK PTHRALADGD TVYCEILGSA
tylosin	ALSPDGRCHT FDARANGYVR	GE GGGAVV LK PLDAALADGD RVYCVIKGGA
301		350
niddam...	TGNDGGGPGL TVPDRA GQEA	VLRAACDQAG VR PADV RFVE LHGTGTPAGD
platenol.	VGNDGGGPGL TAPDREGQEA	VLRAACAQAR VDPAEVRFVE LHGTGTPVGD
monensin	VNSDGT TDGI TLPSGQAQ QD	V VRLACRAR ITPDQVQYVE LHGTGTPVGD
oleandom	LNNDGATEGL TVPSARA QAD	VLRQAWERAR VAPTDVQYVE LHGTGTPAGD
tylosin	VNNNDGGGASL TTPDREA QEA	VLRQAYRAG VSTGAVRYVE LHGTGTRAGD

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Fig 4B

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751	800
niddam...	HG.GAMLSVQ AAEHLDQLA HTHG..VEIA AVNGPTHCVL SGPRTALEET
platenol.	VG.GGMWSVG ASESVVRGVV EGLGEWSVA AVNGPRSVVL SGDVGVLESV
monensin	AP.GAMAAWQ ATADEAAEQL AGHERHVTVA AVNGPDSVVV SGDRATVDEL
oleandom	GG.GVMLSVQ APESEVAPLL LGREAHVGLA AVNGPDAVVV SGERGHVAAI
tylosin	AGRGMAMAAPV LPAGEVEAGL AKWPGVEVA AVNGPASTVV SGDRRAVAGY
801	850
niddam...	AQHLREQNVR HTWLKVSHAF HSALMDPMLG AFRDTLNTLN Y..QPPTIPL
platenol.	VASLMGDGVE YRRLDVSHGF HSVLMEPVLG EFRGVVESLE FGRVRPGVVV
monensin	TAAWRGRGRK AHHLKVSHAF HSPHMDPILD ELRAVAAGLT FHE..PVIPV
oleandom	EQILRDRGRK SRYLDRVSHAF HSPLMEPVLE EFAEAVAGLT FRA..PTTPL
tylosin	VAVCQAEGVQ ARLIPVVDYAS HSRHVEDLKG ELERVLSGI. .RPRSPRVPV
851	900
niddam...	ISNLTGQIA.DPNHL CTPDYWIDHA RHTVRFADAV QTAHHQGTTT
platenol.	VSGVSGGVV.GSGEL GDPGYWVRHA REAVRFADGV GVVRGLGVGT
monensin	VSNVTGELVT ATATGSGAGQ ADPEYWARHA REPVRFLSGV RGLCERGVTT
oleandom	VSNLTG....APVDDRTM ATPAYWVRHV REAVRGDGII RALGKLGTGS
tylosin	CSTVAGEQPG EPVF.....DAGYWFRNL RNRVEFSAVV GGLLEEHRR
901	950
niddam...	YLEIGPHPTL TTLLHHTL.. DNP..... T TIPTLHRERP
platenol.	LVEVGPHGVL TGMAGECLGA GDDV..... V VVPAMRRGRA
monensin	FVELGPDAPL SAMARDCFPAP.....ADRSRPRPA AIATCRRGRD
oleandom	FLEVGPDGVL TAMARACVTA APEPGHRGEQ GADADAHTAL LLPALRRGRD
tylosin	FIEVSAHPVL V..... HAIHQ TAEAADRSVH ATGTLRRQDD
951	
niddam...	EPETLTQIAIA AVGVRTDGID WAVLCGASRP RRVELPTYAF
platenol.	EREVFEAALA TVFTRDAGLD ATALHTGSTG RRIDLPTTPF
monensin	EVATFLRSLA QAYVRGADVD FTRAYGATAT RRFPPLPTYPF
oleandom	EARSLTEAVA RLHLHGVPMD WTSVLGGDVS .RVPLPTYAF
tylosin	SPHRLLTSTA EAWAHGATLT WDPAL..PPG HLTTLPYTF

niddam: niddamycin; platenol: platenolide I (spiramycin); oleandom: oleandomycin.

FIG. 4C

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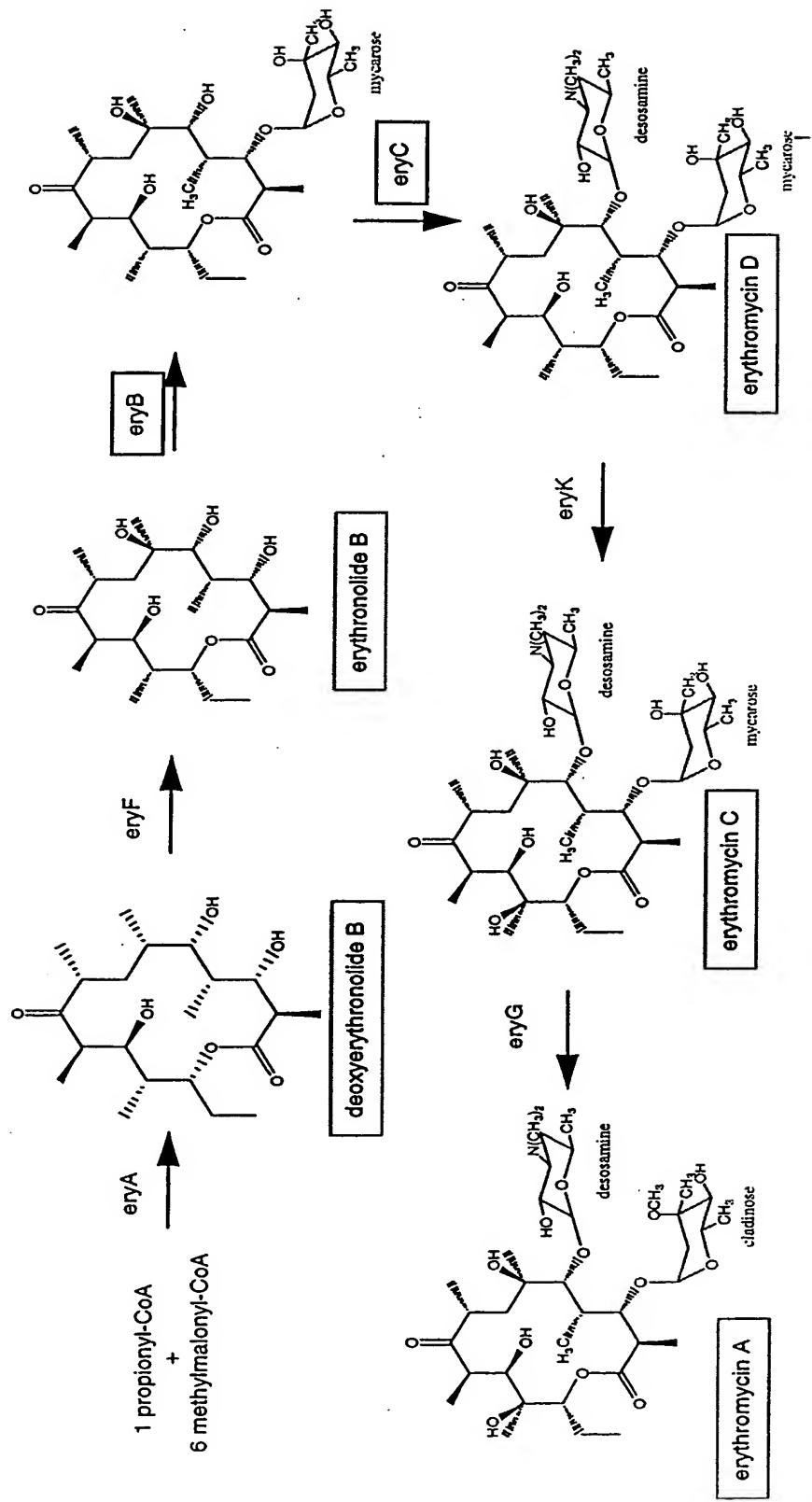


Fig. 5

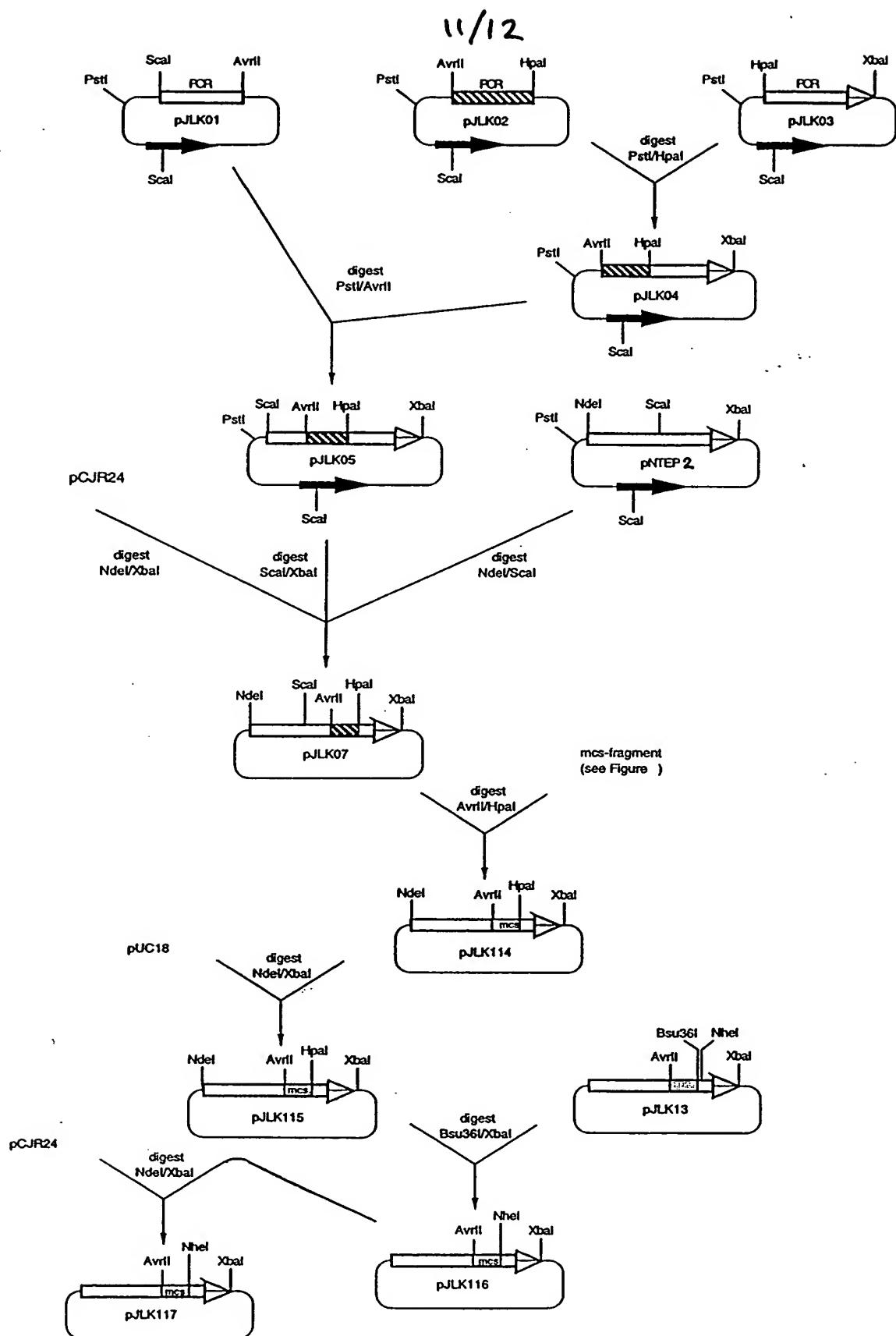


Fig 6

7

forward (Plf):

5'-CTA GGC CGG GCC GGA CTG GTA GAT CTG CCT ACG TAT CCT TTC CAG GGC AAG CGG TTC TGG CTG CAG CCG CGC ACT AGT CCT CGT GAC GAG
GGG GAT GCA TCG AGC CTG AGG GAC CGG T_{3'}

backward (Plb) :

5' -AAC CGG TCC CTC AGG CTC GAT GCA TCT CCC TCG TCA CGA GGA CTA GTC CCG TCC GGC TGC AGC TCG AAC TCG TCA CCC TCG TCA GGC TAC TAC

oligos annealed: